

## AMENDMENTS

### IN THE CLAIMS

Claim 1 is amended to more clearly point out the Claimed invention. Support for the amendment may be found in e.g. original Claim 1 and throughout the specification.

Claim 14 has been amended to correct typographical errors.

## CURRENT STATUS OF ALL CLAIMS IN THE APPLICATION

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1. (previously and currently amended) A method for detecting a plurality of nucleic acid targets in a sample comprising:  
  
hybridizing the sample with at least 50 mediator ~~different~~ nucleic acids and at least 50 different cipher probes immobilized on a microarray ~~substrate~~, wherein each of the mediator nucleic acids has a first subsequence that is complementary with one of the nucleic acid targets and a second subsequence that is complementary with one of the cipher probes; and  
  
detecting at least 50 different nucleic acid targets based upon the hybridization pattern.
2. (original) The method of Claim 1 wherein the mediator nucleic acids and cipher probes are oligonucleotides.
3. (original) The method of Claim 2 wherein the cipher probes do not substantially hybridize with the nucleic acid targets.
4. (previously amended) The method of Claim 3 wherein the cipher probes do not substantially hybridize with any nucleic acid in the sample.
5. (original) The method of Claim 4 wherein the cipher probes are at least 15 bases in length.

6. (original) The method of Claim 5 wherein the cipher probes are at least 20 bases in length.
7. (original) The method of Claim 6 wherein the cipher probes are immobilized at density of at least 400 probes per  $\text{cm}^2$ .
8. (original) The method of Claim 7 wherein the cipher probes are immobilized at a density of at least 1000 probes per  $\text{cm}^2$ .
9. (original) The method of Claim 8 wherein the first subsequences of the mediator oligonucleotides are at least 15 bases in length.
10. (original) The method of Claim 7 wherein the first subsequences are at least 20 bases in length.
11. (original) The method of Claim 10 wherein the second subsequences are at least 15 bases in length.
12. (original) The method of Claim 1 wherein the detecting comprises quantifying the binding of the nucleic acid targets to the cipher probes through the mediator probes.
13. (original) The method of Claim 12 wherein the sample comprises a pool of mRNAs.

14. (currently amended) The method of Claim 12 wherein the sample comprises a pool of ~~is a pool of~~ RNAs in vitro transcribed from a pool of cDNAs.
15. (original) The method of Claim 12 wherein the pool of target nucleic acids is amplified from a biological sample by an in vivo or an in vitro method.
16. (original) The method of Claim 12 wherein pool of target nucleic acids comprises fluorescently labeled nucleic acids.
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COD'f. 17. (original) The method of Claim 12 wherein the cipher probes are synthesized in the 5'-3' direction on the substrate.
18. (original) The method of Claim 17 wherein the cipher probes are synthesized using photo-directed synthesis.
19. (original) The method of Claim 12 wherein the cipher probes are synthesized in the 3'-5' direction on the substrate.
20. (original) The method of Claim 19 wherein the cipher probes are synthesized using photo-directed synthesis.

21. (original) The method of Claim 12 wherein there are at least 3 mediator oligonucleotides and 3 corresponding cipher probes for each of the nucleic acid targets.
22. (original) The method of Claim 21 wherein there are at least 5 mediator oligonucleotides and 5 corresponding cipher probes for each of the nucleic acid targets.
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COO't. 23. (original) The method of Claim 21 wherein there are at least 10 mediator oligonucleotides and 10 corresponding cipher probes for each of the nucleic acid targets.
24. (original) The method of Claim 23 wherein there are at least 20 mediator oligonucleotides and 20 corresponding cipher probes for each of the nucleic acid targets.
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